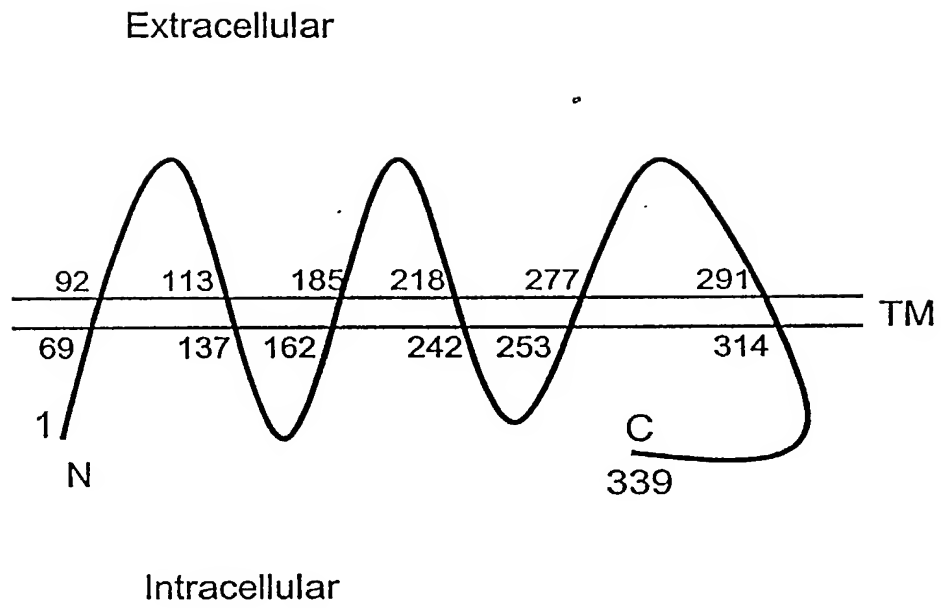


FIG. 1A

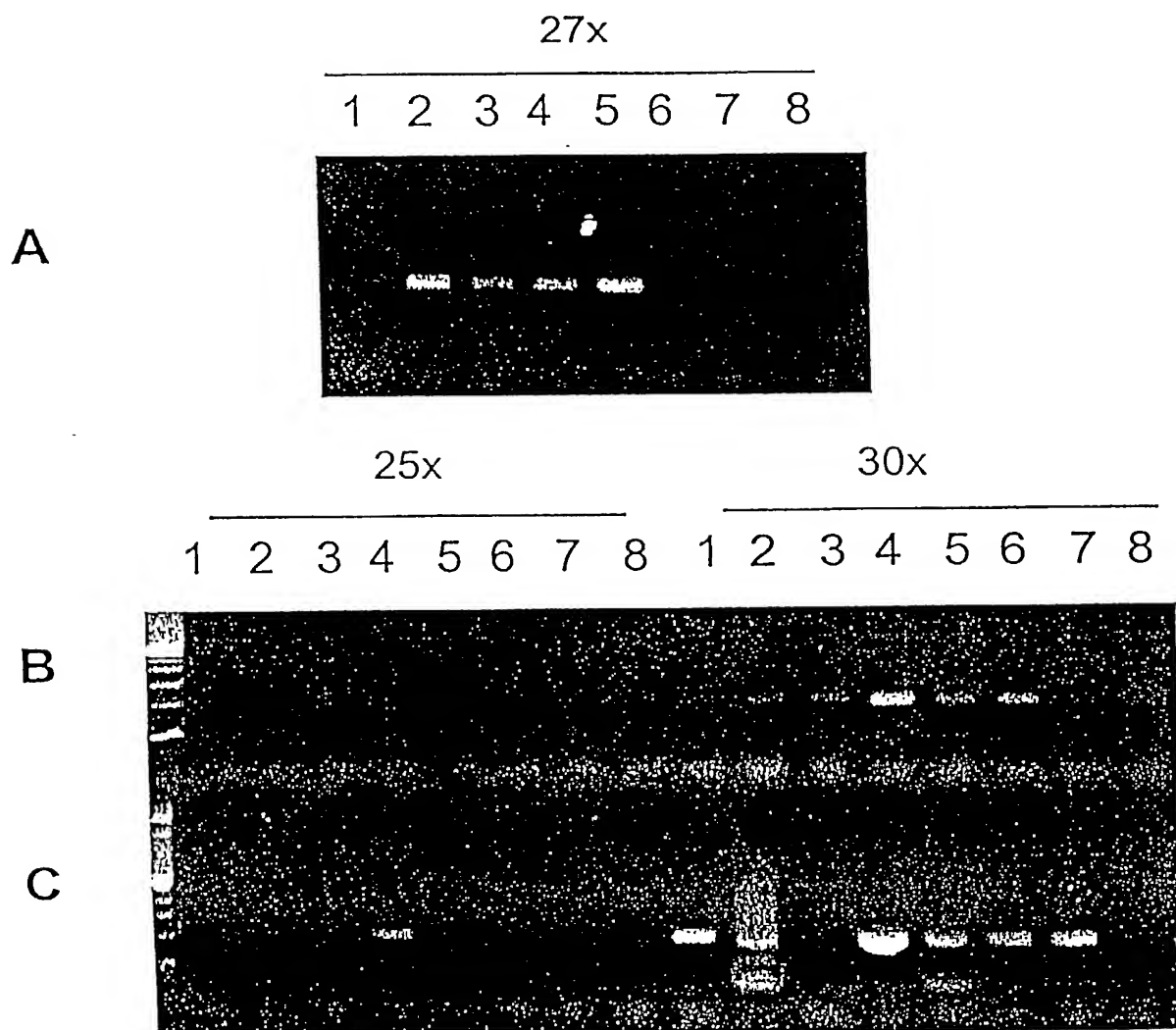
(SEQ ID NO:1)																					
(SEQ ID NO:2)																					
1	↓	GAG	ACT	CAC	GGT	CAA	GCT	AAG	GCG	AAG	AGT	GGG	TGG	CTG	AAG	CCA	TAC	TAT	TTT	ATA	GAA
61	→	TTA	ATG	GAA	AGC	AGA	AAA	GAC	ATC	ACA	AAC	CAA	GAA	GAA	CTT	TGG	AAA	ATG	AAG	CCT	AGG
121		R	N	L	E	E	D	D	Y	L	H	K	D	T	G	E	T	S	M	L	K
181		AGA	AAT	TTA	GAA	GAA	GAC	GAT	TAT	TTG	CAT	AAG	GAC	ACG	GGA	GAG	ACC	AGC	ATG	CTA	AAA
241		R	P	V	L	L	H	L	H	Q	T	A	H	A	D	E	F	D	C	P	S
301		AGA	CCT	GTG	CTT	TTG	CAT	TTG	CAC	CAA	ACA	GCC	CAT	GCT	GAT	GAA	TTT	GAC	TGC	CCT	TCA
361		E	L	Q	H	T	Q	E	L	F	P	Q	W	H	L	P	I	K	I	A	A
421		GAA	CTT	CAG	CAC	ACA	CAG	GAA	CTC	TTT	CCA	CAG	TGG	CAC	TTG	CCA	ATT	AAA	ATA	GCT	AAA
481		I	I	A	S	L	T	F	L	Y	T	L	L	R	E	V	I	H	P	L	A
541		ATT	ATA	GCA	TCT	CTG	ACT	TTT	CTT	TAC	ACT	CTT	CTG	AGG	GAA	GTA	ATT	CAC	CCT	TTA	GCA
601		T	S	H	Q	Q	Y	F	Y	K	I	P	I	L	V	I	N	K	V	L	P
661		ACT	TCC	CAT	CAA	CAA	TAT	TTT	TAT	AAA	ATT	CCA	ATC	CTG	GTC	ATC	AAC	AAA	GTC	TTG	CCA
721		M	V	S	I	T	L	L	A	L	V	Y	L	P	G	V	I	A	A	I	V
781		ATG	GTT	TCC	ATC	ACT	CTC	TTG	GCA	TTG	GTT	TAC	CTG	CCA	GGT	GTG	ATA	GCA	GCA	ATT	GTC
841		Q	L	H	N	G	T	K	Y	K	K	F	P	H	W	L	D	K	W	M	L
901		CAA	CTT	CAT	AAT	GGA	ACC	AAG	TAT	AAG	AAG	TTT	CCA	CAT	TGG	TTG	GAT	AAG	TGG	ATT	TTA
961		T	R	K	Q	F	G	L	L	S	F	F	F	A	V	L	H	A	I	Y	S
1021		ACA	AGA	AAG	CAG	TTT	GGG	CTT	CTC	AGT	TTC	TTT	TTT	GCT	GTA	CTG	CAT	GCA	ATT	TAT	AGT
1081		L	S	Y	P	M	R	R	S	Y	R	Y	K	L	L	N	W	A	Y	Q	Q
1141		CTG	TCT	TAC	CCA	ATG	AGG	CGA	TCC	TAC	AGA	TAC	AAG	TTG	CTA	AAC	TGG	GCA	TAT	CAA	CAG
		V	Q	Q	N	K	E	D	A	W	I	E	H	D	V	W	R	M	E	I	Y
		GTC	CAA	CAA	AAT	AAA	GAA	GAT	GCC	TGG	ATT	GAG	CAT	GAT	GTT	TGG	AGA	ATG	GAG	ATT	TAT
		V	S	L	G	I	V	G	L	A	I	L	A	L	L	A	V	T	S	I	P
		GTG	TCT	CTG	GGA	ATT	GTG	GGA	TTG	GCA	ATA	CTG	GCT	CTG	TTG	GCT	GTG	ACA	TCT	ATT	CCA
		S	V	S	D	S	L	T	W	R	E	F	H	Y	I	Q	S	K	L	G	I
		TCT	GTG	AGT	GAC	TCT	TTG	ACA	TGG	AGA	GAA	TTT	CAC	TAT	ATT	CAG	AGC	AAG	CTA	GGA	ATT
		V	S	L	L	L	G	T	I	H	A	L	I	F	A	W	N	K	W	I	D
		GTT	TCC	CTT	CTA	CTG	GGC	ACA	ATA	CAC	GCA	TTG	ATT	TTT	GCC	TGG	AAT	AAG	TGG	ATA	GAT
		I	K	Q	F	V	W	Y	T	P	P	T	F	M	I	A	V	F	L	P	I
		ATA	AAA	CAA	TTT	GTA	TGG	TAT	ACA	CCT	CCA	ACT	TTT	ATG	ATA	GCT	GTT	TTC	CTT	CCA	ATT
		V	V	L	I	F	K	S	I	L	F	L	P	C	L	R	K	K	I	L	K
		GTT	GTC	CTG	ATA	TTT	AAA	AGC	ATA	CTA	TTC	CTG	CCA	TGC	TTG	AGG	AAG	AAG	ATA	CTG	AAG
		I	R	H	G	W	E	D	V	T	K	I	N	K	T	E	I	C	S	Q	L
		ATT	AGA	CAT	GGT	TGG	GAA	GAC	GTC	ACC	AAA	ATT	AAC	AAA	ACT	GAG	ATA	TGT	TCC	CAG	TTG
		TAG	AAT	TAC	TGT	TTA	CAC	ACA	TTT	TTG	TTC	AAT	ATT	GAT	ATA	TTT	TAT	CAC	CAA	CAT	TTC
		AAG	TTT	GTA	TTT	GTT	AAT	AAA	ATG	ATT	ATT	CAA	GGA	AAA	AAA	AAA	AAA	AAA	AAA	AA	

**FIG. 1B**





**FIG. 2**



**Panels:**

**A**

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

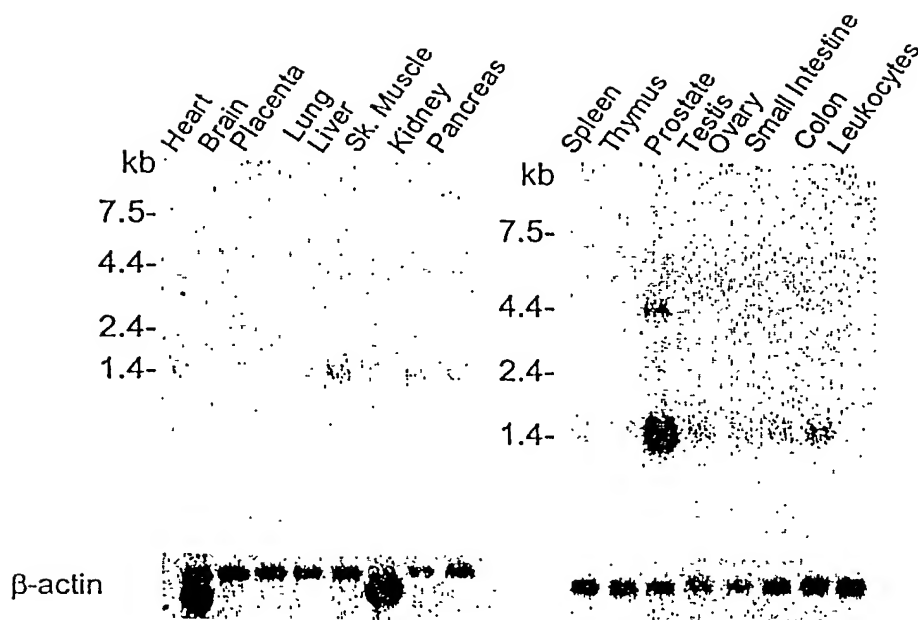
**B**

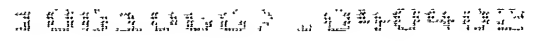
1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

**C**

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A



[illegible]

GGGGCCCGCACCTCTGGGCAGCAGCGGACCCGAGACTCACGGTCAAGCTAAGGCCGAAGAGTGGGTGGCTGAAGCC  
ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAATGAAGCCTAGG  
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC  
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACA  
GTGGCACTTGCCAATTAATAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT  
CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG  
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTCATAATGGAACCAA  
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT  
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT  
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT  
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG  
AGAGAATTTCACTATATTCAGGTAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT  
ATAGAATATGTTGACTTTACCCATAAAAAATAACAAATGTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT  
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAATAAAGGCAT  
TAAATATTCTTTGTTTTTTTTTTTTTTGTTTGTGTTTTTTGTTTGTGTTTTTTGAGATGAAGTCTCG  
CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATT  
TCTTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTGTATTTTAGTA  
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCACCTCGGCCTCCC  
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT  
GCTACCCATCTAATGTGATATTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACC  
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGAAA  
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT  
ACTTACTCACTTGAAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT  
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAA

FIG. 4-2



FIG. 5

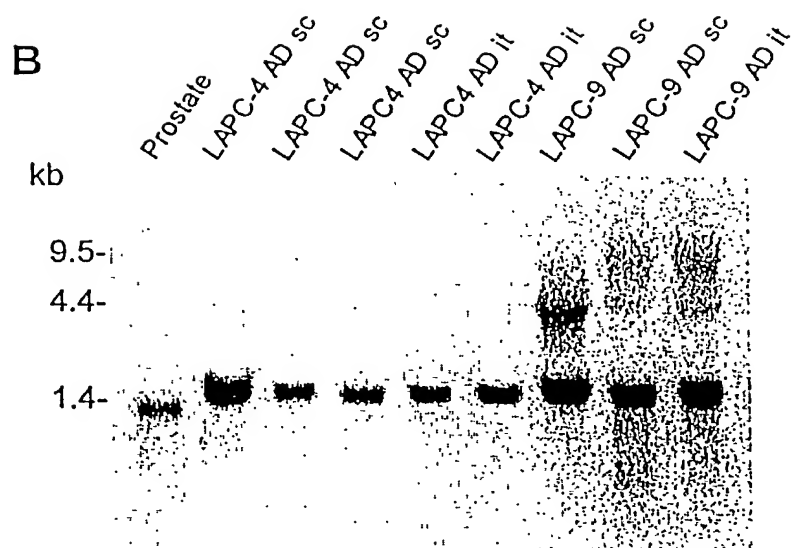
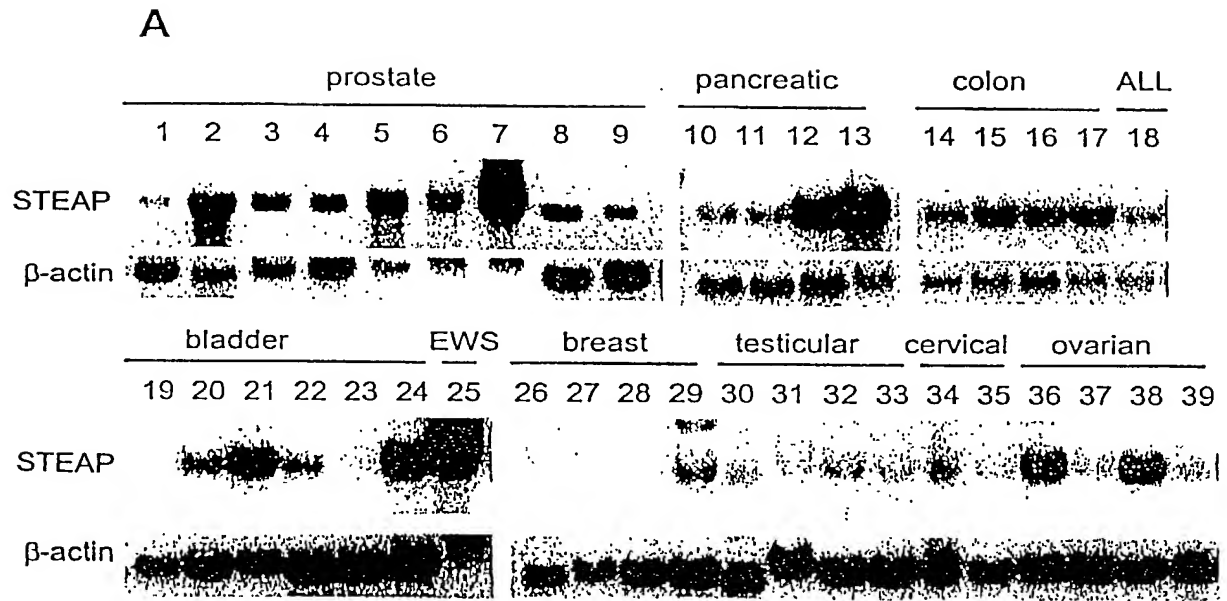
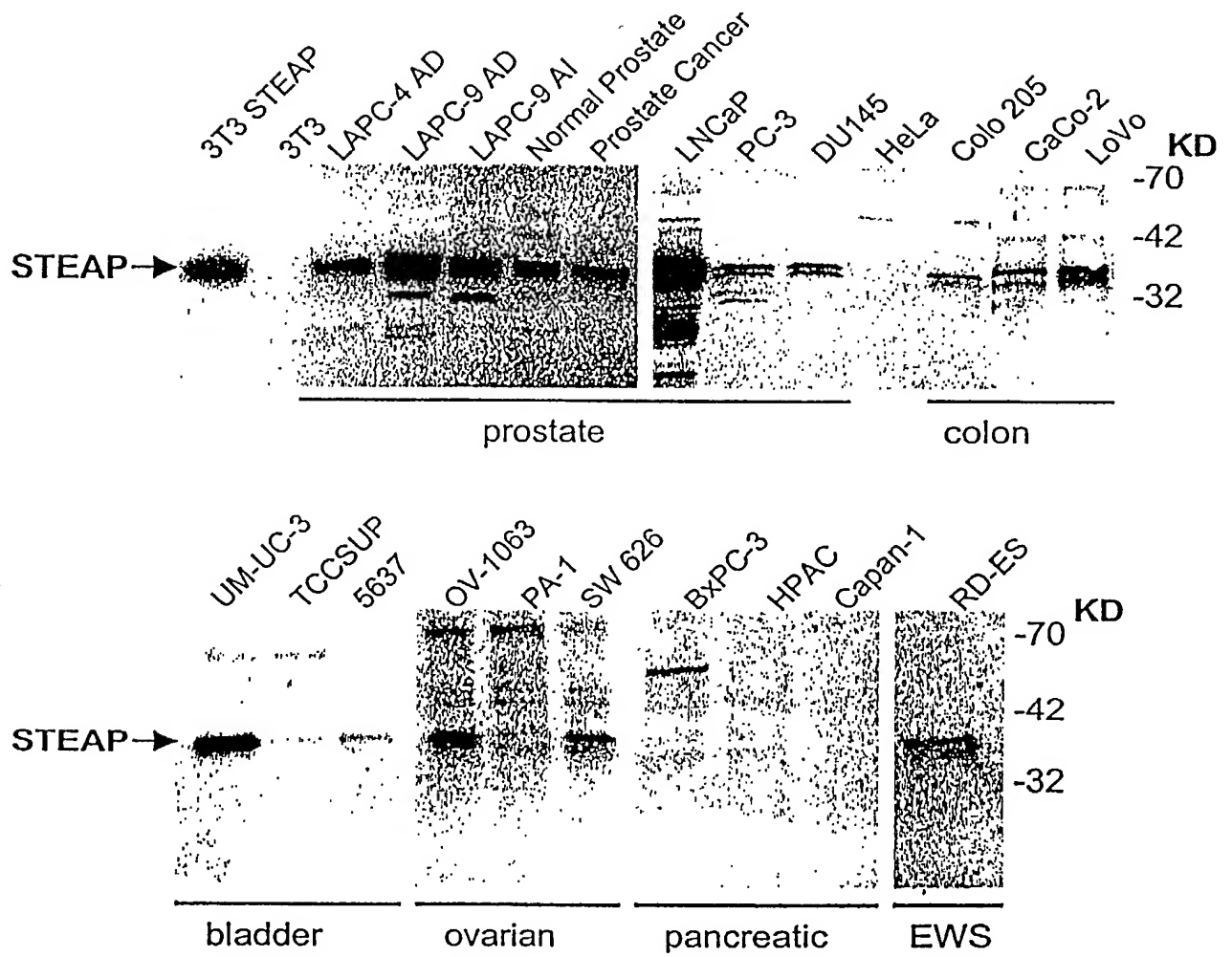
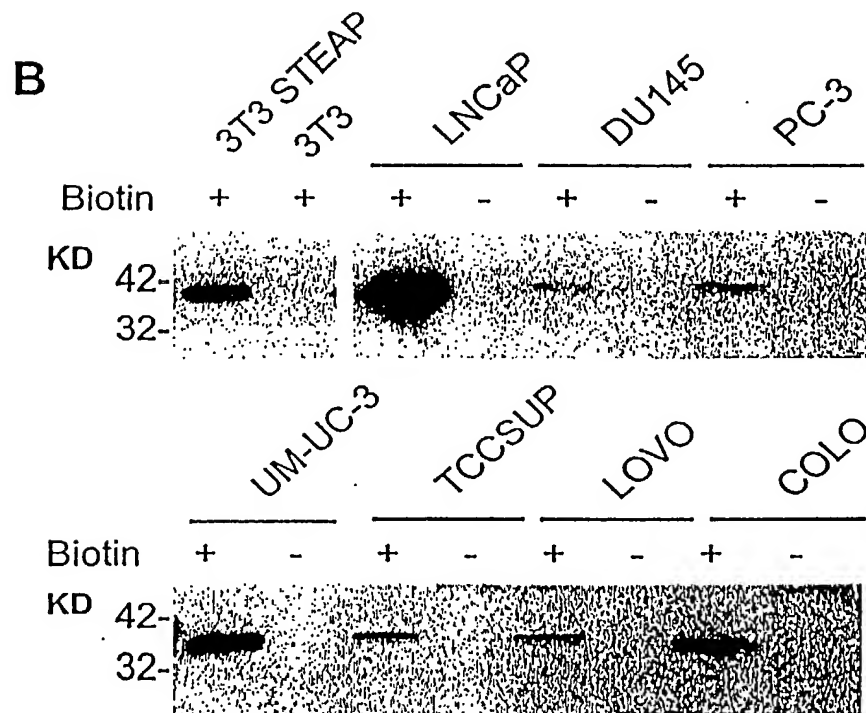
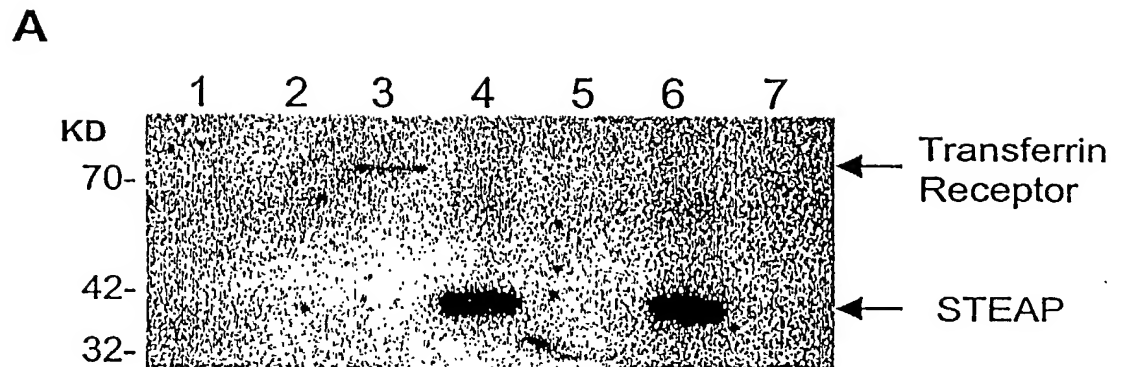


FIG. 6



**FIG. 7**



• • •

			10			19			28			37			46			55
5'	GAC	TTT	TAC	AAA	ATT	CCT	ATA	GAG	ATT	GTG	AAT	AAA	ACC	TTA	CCT	ATA	GTT	GCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Asp	Phe	Tyr	Lys	Ile	Pro	Ile	Glu	Ile	Val	Asn	Lys	Thr	Leu	Pro	Ile	Val	Ala
		64				73			82			91			100			109
	ATT	ACT	TTG	CTC	TCC	CTA	GTA	TAC	CTC	GCA	GGT	CTT	CTG	GCA	GCT	GCT	TAT	CAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ile	Thr	Leu	Leu	Ser	Leu	Val	Tyr	Leu	Ala	Gly	Leu	Leu	Ala	Ala	Ala	Tyr	Gln
		118				127			136			145			154			163
	CTT	TAT	TAC	GGC	ACC	AAG	TAT	AGG	AGA	TTT	CCA	CCT	TGG	TTG	GAA	ACC	TGG	TTA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Tyr	Tyr	Gly	Thr	Lys	Tyr	Arg	Arg	Phe	Pro	Pro	Trp	Leu	Glu	Thr	Trp	Leu
		172				181			190			199			208			217
	CAG	TGT	AGA	AAA	CAG	CTT	GGA	TTA	CTA	AGT	TTT	TTC	TTC	GCT	ATG	GTC	CAT	GTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Gln	Cys	Arg	Lys	Gln	Leu	Gly	Leu	Leu	Ser	Phe	Phe	Phe	Ala	Met	Val	His	Val
		226				235			244			253			262			271
	GCC	TAC	AGC	CTC	TGC	TTA	CCG	ATG	AGA	AGG	TCA	GAG	AGA	TAT	TTG	TTT	CTC	AAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser	Glu	Arg	Tyr	Leu	Phe	Leu	Asn
		280				289			298			307			316			325
	ATG	GCT	TAT	CAG	CAG	GTT	CAT	GCA	AAT	ATT	GAA	AAC	TCT	TGG	AAT	GAG	GAA	GAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Met	Ala	Tyr	Gln	Gln	Val	His	Ala	Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu
		334				343			352			361			370			379
	GTT	TGG	AGA	ATT	GAA	ATG	TAT	ATC	TCC	TTT	GGC	ATA	ATG	AGC	CTT	GGC	TTA	CTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Val	Trp	Arg	Ile	Glu	Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu
		388				397			406			415			424			433
	TCC	CTC	CTG	GCA	GTC	ACT	TCT	ATC	CCT	TCA	GTG	AGC	AAT	GCT	TTA	AAC	TGG	AGA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Leu	Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp	Arg
		442				451			460			469			478			487
	GAA	TTC	AGT	TTT	ATT	CAG	TCT	ACA	CTT	GGA	TAT	GTC	GCT	CTG	CTC	ATA	AGT	ACT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu	Leu	Ile	Ser	Thr
		496				505			514									
	TTC	CAT	GTT	TTA	ATT	TAT	GGA	TGG	AAA	CGA	GCT	3' (SEQ ID NO:7)						
	---	---	---	---	---	---	---	---	---	---	---							
	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala	(SEQ ID NO:8)						

## FIG. 10

STEAP-2, AA508880 (NCI\_CGAP Pr6)

ggtcgacttttcctttattcctttgtcagagatctgattcatccatatgctagaaaccaacagagtgacttttaca  
aaattcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctagtataccttgcagg  
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttgggttggaacctgggtta  
cagtgtagaaaacagcttggattactaagttgtttcttcgctatgggtccatgttgctacagcctctgcttaccca  
tgagaaggtcagagagat (SEQ ID NO:9)

STEAP-2, 98P4B6 SSH fragment

TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAAGTGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAAGCG  
GCTGCCATTACATTCCCTCAGCTGTCCTTGCAAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC  
TCCTCAAAGGAAGGCAGCATGTGTCCTTTT (SEQ ID NO:10)

AI139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttgggtttt  
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcactggagagagttccgatttgt  
ccagtcctaaactgggttatttgacctgatcttgtgtacagccacacccctgggtgtacgggtgggaagagattcctc  
agcccttcaaactcagatgggtatcttctgcagcctacgtgttagggcttatcatccttgactgtgctgggtga  
tcaagtttgtcctaataatcatgccatgtgtagacaacaccccttacaaggatccgcccagggtgggaaaggaaactcaaa  
acactagaaaaagcattgaatggaaaatcaatattttaaacaaggttcaatttagctggaaaaaa (SEQ ID NO:11)

R80991 (placental EST)

ggccgcggcancgcctacgacctgggtcaacctggcagtcagggtcttggccanacaagagccacctctgggtg  
aaggaggagggtctggcgatggagatctacctctccctgggagtgctggccctcggcacggtgtccctgctggcgg  
tgacctcactgccgtccattgcaaaactcgctcaactggaggagttcagcttcggtcagtcctcactgggcttgg  
ggcctcgtgctgagcacactncacacgctcacctacgggtggaccgcgccttcgaggagagccgctacaagttc  
tacctnctcccaccttcacgntcacgctgctgggtgccctgcgttcggttcacctcctgggccaaggccctggttntac  
tgccttgcatcagccgnaga (SEQ ID NO:12)

# FIG. 11A

STEAP-1	106	FYKIPILVINKVLPV SITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKMWLTRKQFG
STEAP-2	2	FYKIPIEIVNKTLP IVAITLLSLVYLAGLLAAAYQLYYGTYRRFPFWLETWLQCRKQLG
		*****    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *
STEAP-1	166	LLSFFFAVLHAIYSLSPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIV
STEAP-2	62	LLSFFFAMVHVAYSLCLPMRRSERYFLN MAYQQVHANIENSWNEEEVWRIEMYISFGIM
		*****    *    *    *    *    *    *    *    *    *    *    *    *    *    *
		(Portion of SEQ ID NO:2)
		↓
STEAP-1	226	GLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLGLTIHALIFAWNK
STEAP-2	122	SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
		*    *    *****    *    *****    *    *    *    *    *    *    *    *    *
		↑
		(Portion of SEQ ID NO:8)

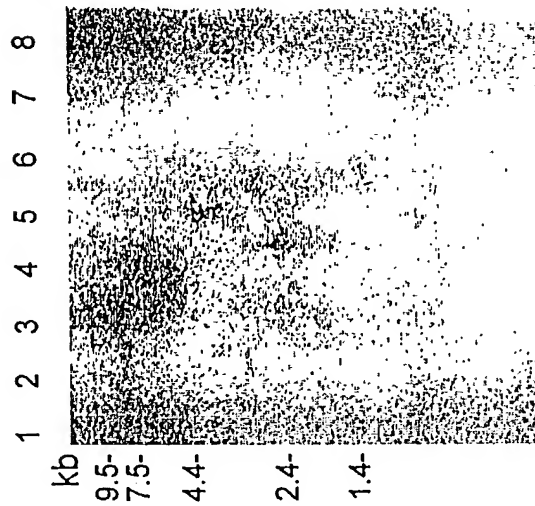
[illegible]

1	15 16	30 31	45 46	60 61	75 76	90
STEAP-1	MESRKOITNQEEAK	MKPRRNLEEDDYLHK	DGGETSMLARFVLH	LHQTAHADEFDCPSE	LQHTQELFPQWHLPI	KIAAIIASLTFYTL
STEAP-2	-----	-----	-----	-----	-----	-----
STEAP-3	-----	-----	-----	-----	-----	-----
STEAP-4	-----	-----	-----	-----	-----	-----
91	105 106	120 121	135 136	150 151	165 166	180
STEAP-1	LREVIHPLATSEQY	FYKIPILVINKVLPW	VSITLLALVYLPGL	AAIVQLHNGTKYKGF	PPWLDKMWLTKRQFG	LLSFPFANLHAIYST
STEAP-2	-----D	FYKIPISLVNKLPI	VAITLLSLVYLAGLI	AAAYQLAYGTKYRRF	PPWLEFWLQCRKQLG	LLSFPFAMVHVAYSL
STEAP-3	-----	-----	-----	-----	-----	-----
STEAP-4	-----	-----	-----	-----	-----	-----
181	195 196	210 211	225 226	240 241	255 256	270
STEAP-1	SYEMRRSRYJKENW	AYQOVQONKEDAWIE	HDVWRMEIYVSLGIV	GLAIIALLAVTSIPS	VSPSLTWREHFYIQS	KLGIIVSLLGCTIHAI
STEAP-2	CLPMRRSRYLPLNM	AYQOVQENIENSWE	ESVWRIEATYISFGIM	SLGLLSLLAVTSIPS	VSNALNWRRESFIQS	TLGYVALLISTPFTL
STEAP-3	-----	-----KENPPST	SSAWLSDSYVALGIL	GPFLFVLIGITSIPS	VSNAVNWREPEREVQS	KLGYLTLLICTAHTL
STEAP-4	-----ATTKSTW	QSSRSWPXKSHLWK	EEVWRMEIYVSLGVL	ALGTLSSLAVTSIPS	IANSINWREPEREVQS	SLGEVAVVLSLTHLI
271	285 286	300 301	315 316	330 331	345 346	360
STEAP-1	IFAMNKNWIDIKQFVW	YTPPTFMIAVFLPIV	VLIIFKSIILFPLCLPK	KILKIRHGWEDVTKI	NKTEICSQL	339 (SEQ ID NO:2)
STEAP-2	TYGWTGA	-----	-----	-----	-----	173 (SEQ ID NO:8)
STEAP-3	YVGKRFSPSNLW	YLPAAVYVGLLIIPCT	VLVIKFVLIDPCVDN	TLTRIRQGWERNSKH	-----	128 (Portion of SEQ ID NO:2)
STEAP-4	TYGWTARAFEESEYKF	YLPPTFTXTLLVPCV	RSSWAKALFXLPCIQ	P-----	-----	128 (Portion of SEQ ID NO:8)



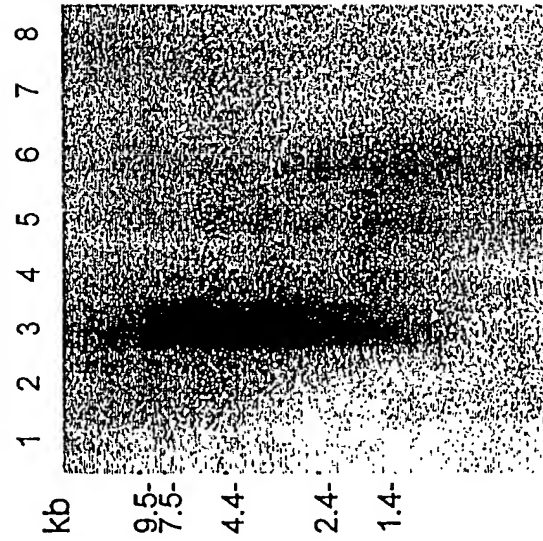


FIG. 15A



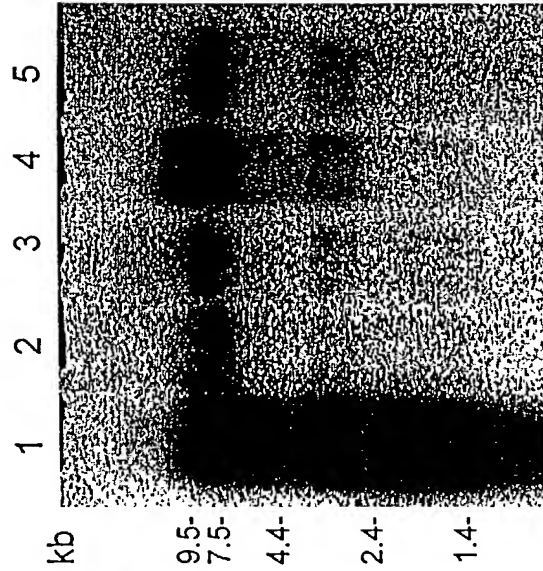
1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas

FIG. 15B



1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

FIG. 15C



1. Prostate
2. LAPC-4 AD
3. LAPC-4 AI
4. LAPC-9 AD
5. LAPC-9 AI

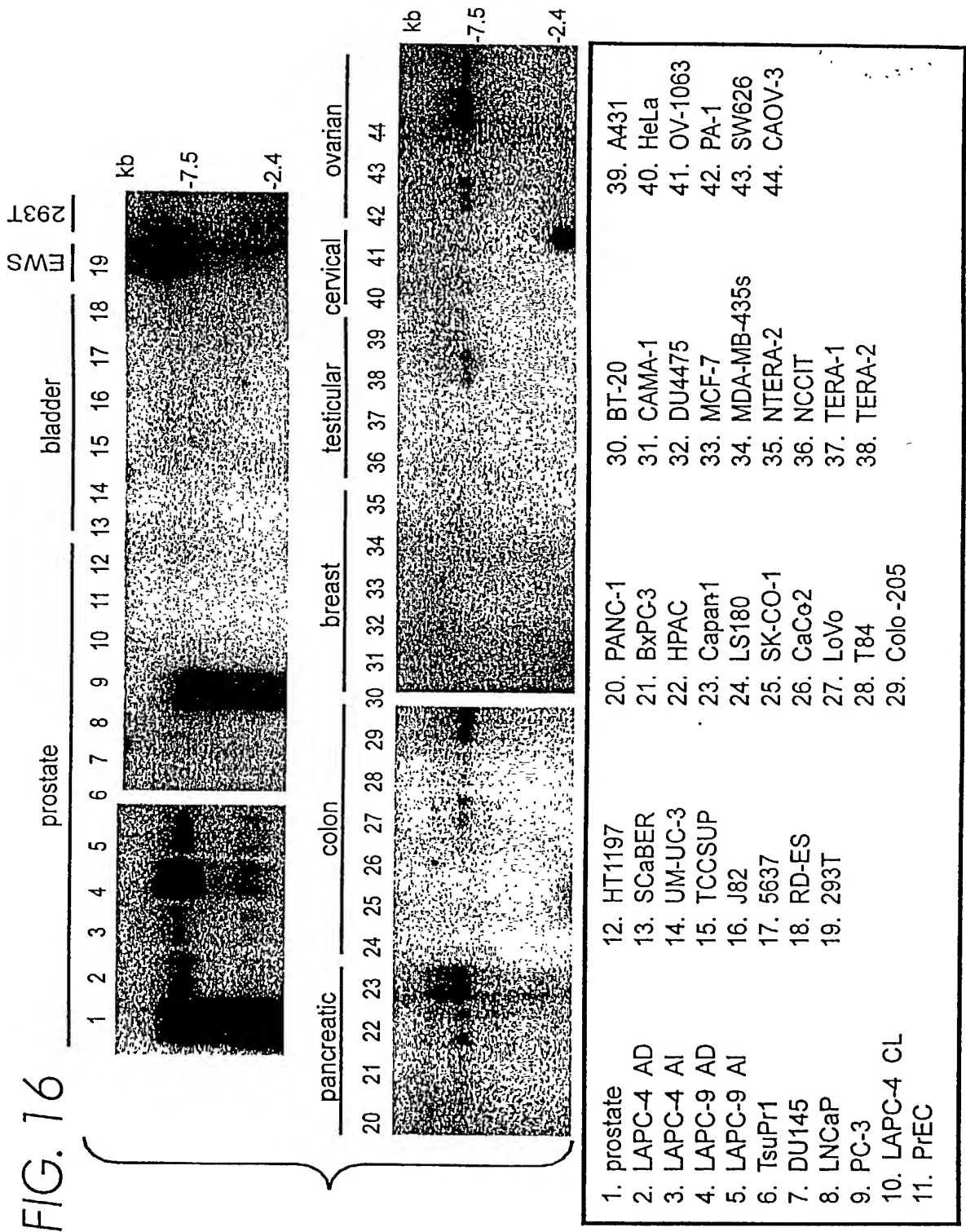
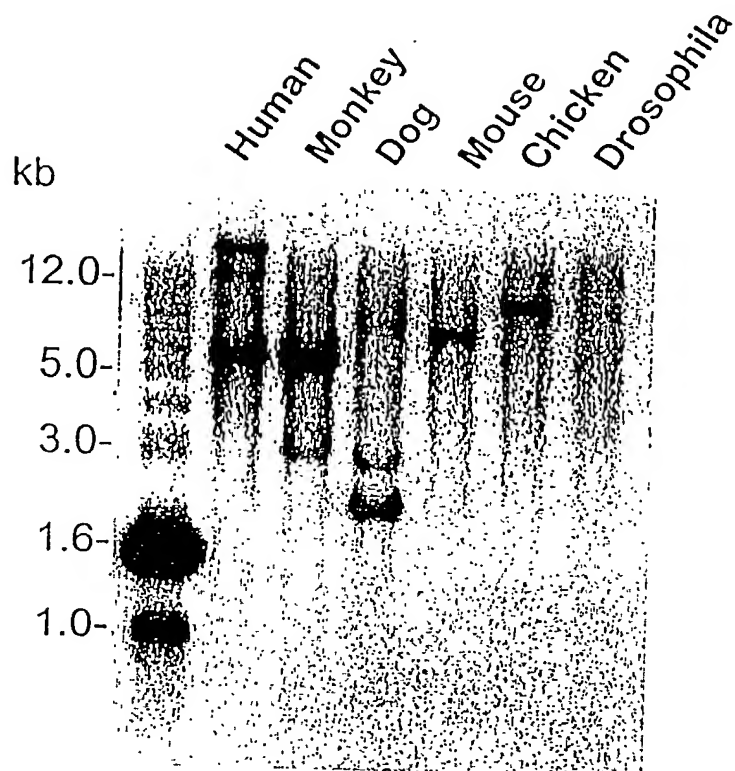
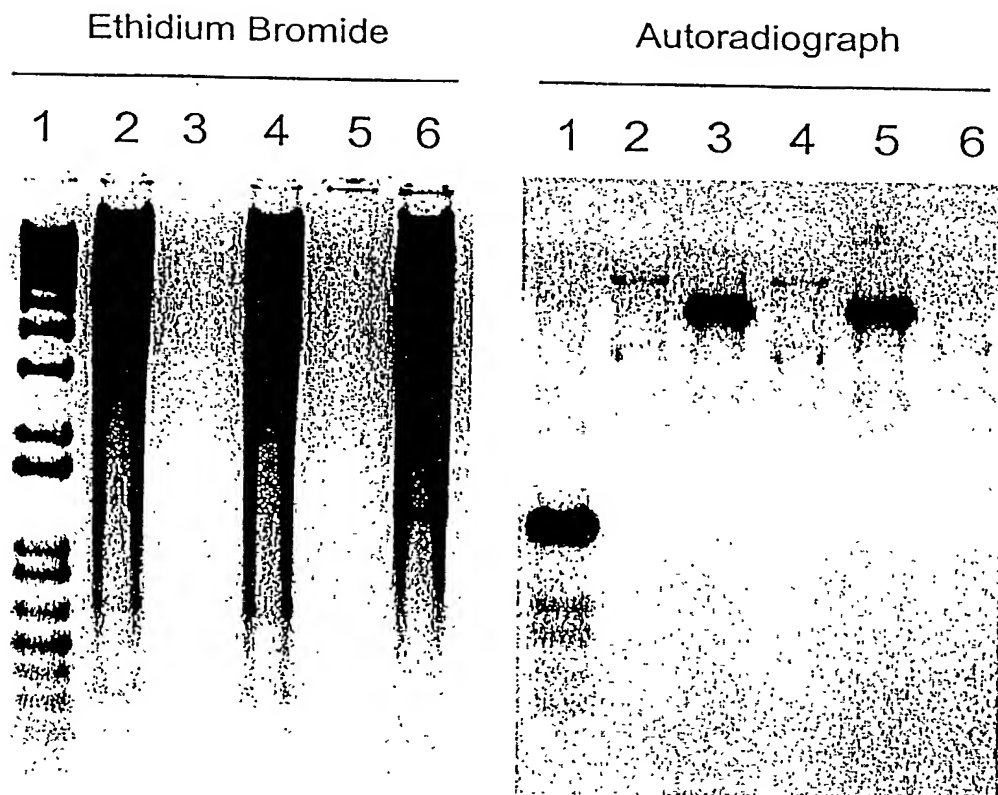




FIG. 19



**FIG. 20****Lanes**

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3